RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/517,491A_
Source: _/FW/6_
Date Processed by STIC: _4/12/05_

ENTERED

IFW16

```
  4 <110> APPLICANT: Berlin, Vivian
  5        Chiu, Maria Isabel
  6        Cottarel, Guillaume
  7        Damagnez, Veronique
  9 <120> TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
 12 <130> FILE REFERENCE: APBI-P06-036
 14 <140> CURRENT APPLICATION NUMBER: US 09/517,491A
 15 <141> CURRENT FILING DATE: 2000-03-02
 17 <150> PRIOR APPLICATION NUMBER: US 08/360,144
 18 <151> PRIOR FILING DATE: 1994-12-20
 20 <150> PRIOR APPLICATION NUMBER: US 08/250,795
 21 <151> PRIOR FILING DATE: 1994-05-27
 23 <160> NUMBER OF SEQ ID NOS: 35
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 486
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Mouse
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)...(486)
 36 <400> SEQUENCE: 1
 37 ctc acc cgt cac aat gca gcc aac aag atc ttg aag aac atg tgt gaa    48
 38 Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu
 39 1               5                  10                  15
 41 cac agc aac acg ctg gtc cag cag gcc atg atg gtg agt gaa gag ctg    96
 42 His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu
 43              20                  25                  30
 45 att cgg gta gcc atc ctc tgg cat gag atg tgg cat gaa ggc ctg gaa   144
 46 Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu
 47          35                  40                  45
 49 gag gca tct cgc ttg tac ttt ggg gag agg aac gtg aaa ggc atg ttt   192
 50 Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
 51      50                  55                      60
 53 gag gtg ctg gag ccc ctg cat gct atg atg gaa cgg ggt ccc cgg act   240
 54 Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr
 55  65                  70                  75                  80
 57 ctg aag gaa aca tcc ttt aat cag gca tat ggc cga gat tta atg gag   288
 58 Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
 59                  85                  90                  95
 61 gca caa gaa tgg tgt cga aag tac atg aag tcg ggg aac gtc aag gac   336
 62 Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
 63                 100                 105                 110
```

```
65 ctc acg caa gcc tgg gac ctc tac tat cac gtg ttc aga cgg atc tca      384
66 Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
67         115                 120                 125
69 aag cag cta ccc cag ctc aca tcc ctg gag ctg cag tat gtg tcc ccc      432
70 Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro
71      130                 135                 140
73 aaa ctt ctg atg tgc cga gac ctt gag ttg gct gtg cca gga aca tac      480
74 Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr
75 145                 150                 155                 160
77 gac ccc                                                              486
78 Asp Pro
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 162
84 <212> TYPE: PRT
85 <213> ORGANISM: Mouse
87 <400> SEQUENCE: 2
88 Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu
89 1               5                   10                  15
90 His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu
91             20                  25                  30
92 Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu
93         35                  40                  45
94 Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
95      50                  55                  60
96 Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr
97 65                  70                  75                  80
98 Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
99              85                  90                  95
100 Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
101             100                 105                 110
102 Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
103         115                 120                 125
104 Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro
105      130                 135                 140
106 Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr
107 145                 150                 155                 160
108 Asp Pro
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 40
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: oligonucleotide
120 <400> SEQUENCE: 3
121 gggtttggaa ttcctaataa tgtctgtaca agtagaaacc                          40
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 34
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
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RAW SEQUENCE LISTING   DATE: 04/12/2005
PATENT APPLICATION: US/09/517,491A   TIME: 14:20:54

Input Set : A:\ABPI-P06-036.TXT
Output Set: N:\CRF4\04122005\I517491A.raw

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128 <220> FEATURE:
129 <223> OTHER INFORMATION: oligonucleotide
131 <400> SEQUENCE: 4
132 gggtttcggg atcccgtcat tccagtttta gaac                        34
134 <210> SEQ ID NO: 5
135 <211> LENGTH: 348
136 <212> TYPE: DNA
137 <213> ORGANISM: Homo sapiens
139 <220> FEATURE:
140 <221> NAME/KEY: CDS
141 <222> LOCATION: (14)...(325)
143 <400> SEQUENCE: 5
144 ggaattccta ata atg tcc gta caa gta gaa acc atc tcc cca gga gac   49
145              Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp
146               1               5               10
148 ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg gtg cac tac acc   97
149 Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr
150          15              20              25
152 ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc cgt gac cgt aac  145
153 Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn
154      30              35              40
156 aag ccc ttt aag ttt atg cta ggc aag cag gag gtg atc cga ggc tgg  193
157 Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp
158  45              50              55              60
160 gaa gaa ggg gtt gcc cag atg agt gtg ggt cag cgt gcc aaa ctg act  241
161 Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr
162              65              70              75
164 ata tct cca gat tat gcc tat ggt gcc act ggg cac cca ggc atc atc  289
165 Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile
166          80              85              90
168 cca cca cat gcc act ctc gtc ttc gat gtg gag ctt ctaaaactgg       335
169 Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
170          95              100
172 aatgacggga tcc                                                  348
174 <210> SEQ ID NO: 6
175 <211> LENGTH: 104
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
179 <400> SEQUENCE: 6
180 Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
181  1               5               10              15
182 Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
183          20              25              30
184 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
185          35              40              45
186 Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
187      50              55              60
188 Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
189  65              70              75              80
```

```
190 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
191              85                  90                  95
192 Thr Leu Val Phe Asp Val Glu Leu
193             100
196 <210> SEQ ID NO: 7
197 <211> LENGTH: 48
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: oligonucleotide
204 <400> SEQUENCE: 7
205 tcgccggaat tcggggcgg aggtggagga gtacaagtag aaaccatc              48
207 <210> SEQ ID NO: 8
208 <211> LENGTH: 34
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: oligonucleotide
215 <400> SEQUENCE: 8
216 gggtttcggg atcccgtcat tccagtttta gaag                           34
218 <210> SEQ ID NO: 9
219 <211> LENGTH: 41
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: oligonucleotide
226 <400> SEQUENCE: 9
227 cgcggatccg cgcattatta cttgttttga ttgattttt g                    41
229 <210> SEQ ID NO: 10
230 <211> LENGTH: 40
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: oligonucleotide
237 <400> SEQUENCE: 10
238 cgcggatccg cgtaaaagca aagtactatc aattgagccg                     40
240 <210> SEQ ID NO: 11
241 <211> LENGTH: 5430
242 <212> TYPE: DNA
243 <213> ORGANISM: Homo sapiens
245 <220> FEATURE:
246 <221> NAME/KEY: CDS
247 <222> LOCATION: (1)...(5427)
249 <400> SEQUENCE: 11
250 ttg gag cac agt ggg att gga aga atc aaa gag cag agt gcc cgc atg    48
251 Leu Glu His Ser Gly Ile Gly Arg Ile Lys Glu Gln Ser Ala Arg Met
252  1               5                  10                  15
254 ctg ggg cac ctg gtc tcc aat gcc ccc cga ctc atc cgc ccc tac atg    96
255 Leu Gly His Leu Val Ser Asn Ala Pro Arg Leu Ile Arg Pro Tyr Met
```

Input Set : **A:\ABPI-P06-036.TXT**
Output Set: **N:\CRF4\04122005\I517491A.raw**

```
256                20                   25                  30
258 gag cct att ctg aag gca tta att ttg aaa ctg aaa gat cca gac cct   144
259 Glu Pro Ile Leu Lys Ala Leu Ile Leu Lys Leu Lys Asp Pro Asp Pro
260         35                   40                   45
262 gat cca aac cca ggt gtg atc aat aat gtc ctg gca aca ata gga gaa   192
263 Asp Pro Asn Pro Gly Val Ile Asn Asn Val Leu Ala Thr Ile Gly Glu
264       50                   55                   60
266 ttg gca cag gtt agt ggc ctg gaa atg agg aaa tgg gtt gat gaa ctt   240
267 Leu Ala Gln Val Ser Gly Leu Glu Met Arg Lys Trp Val Asp Glu Leu
268 65                   70                   75                   80
270 ttt att atc atc atg gac atg ctc cag gat tcc tct ttg ttg gcc aaa   288
271 Phe Ile Ile Ile Met Asp Met Leu Gln Asp Ser Ser Leu Leu Ala Lys
272               85                   90                   95
274 agg cag gtg gct ctg tgg acc ctg gga cag ttg gtg gcc agc act ggc   336
275 Arg Gln Val Ala Leu Trp Thr Leu Gly Gln Leu Val Ala Ser Thr Gly
276             100                  105                  110
278 tat gta gta gag ccc tac agg aag tac cct act ttg ctt gag gtg cta   384
279 Tyr Val Val Glu Pro Tyr Arg Lys Tyr Pro Thr Leu Leu Glu Val Leu
280             115                  120                  125
282 ctg aat ttt ctg aag act gag cag aac cag ggt aca cgc aga gag gcc   432
283 Leu Asn Phe Leu Lys Thr Glu Gln Asn Gln Gly Thr Arg Arg Glu Ala
284       130                  135                  140
286 atc cgt gtg tta ggg ctt tta ggg gct ttg gat cct tac aag cac aaa   480
287 Ile Arg Val Leu Gly Leu Leu Gly Ala Leu Asp Pro Tyr Lys His Lys
288 145                  150                  155                  160
290 gtg aac att ggc atg ata gac cag tcc cgg gat gcc tct gct gtc agc   528
291 Val Asn Ile Gly Met Ile Asp Gln Ser Arg Asp Ala Ser Ala Val Ser
292             165                  170                  175
294 ctg tca gaa tcc aag tca agt cag gat tcc tct gac tat agc act agt   576
295 Leu Ser Glu Ser Lys Ser Ser Gln Asp Ser Ser Asp Tyr Ser Thr Ser
296             180                  185                  190
298 gaa atg ctg gtc aac atg gga aac ttg cct ctg gat gag ttc tac cca   624
299 Glu Met Leu Val Asn Met Gly Asn Leu Pro Leu Asp Glu Phe Tyr Pro
300             195                  200                  205
302 gct gtg tcc atg gtg gcc ctg atg cgg atc ttc cga gac cag tca ctc   672
303 Ala Val Ser Met Val Ala Leu Met Arg Ile Phe Arg Asp Gln Ser Leu
304       210                  215                  220
306 tct cat cat cac acc atg gtt gtc cag gcc atc acc ttc atc ttc aag   720
307 Ser His His His Thr Met Val Val Gln Ala Ile Thr Phe Ile Phe Lys
308 225                  230                  235                  240
310 tcc ctg gga ctc aaa tgt gtg cag ttc ctg ccc cag gtc atg ccc acg   768
311 Ser Leu Gly Leu Lys Cys Val Gln Phe Leu Pro Gln Val Met Pro Thr
312             245                  250                  255
314 ttc ctt aat gtc att cga gtc tgt gat ggg gcc atc cgg gaa ttt ttg   816
315 Phe Leu Asn Val Ile Arg Val Cys Asp Gly Ala Ile Arg Glu Phe Leu
316             260                  265                  270
318 ttc cag cag ctg gga atg ttg gtg tcc ttt gtg aag agc cac atc aga   864
319 Phe Gln Gln Leu Gly Met Leu Val Ser Phe Val Lys Ser His Ile Arg
320             275                  280                  285
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/12/2005
PATENT APPLICATION: US/09/517,491A   TIME: 14:20:55

Input Set : **A:\ABPI-P06-036.TXT**
Output Set: **N:\CRF4\04122005\I517491A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:19; N Pos. 59,64,72,74,89,94,101,137,158,175,190,201,207,210,213,218
Seq#:19; N Pos. 234,243,257,283,286,289,292,314,325,328,335,352,361,380,384
Seq#:19; N Pos. 390,393,403,411,413,427,432,435,440,443,450,452,460,465,480
Seq#:19; N Pos. 482,486,492,515
Seq#:23; N Pos. 27,373,443,461,483,485,507,583,588,593,605,606,607,612,624
Seq#:23; N Pos. 625,626,627,628,630,631,632,635,639,646,652,659,661
Seq#:24; Xaa Pos. 105
Seq#:25; N Pos. 112,148,158,171,178,182,191,194,203,204
Seq#:29; N Pos. 3,9,15
Seq#:30; N Pos. 3,6,21
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VERIFICATION SUMMARY   DATE: 04/12/2005
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```
L:1157 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:1158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
M:341 Repeated in SeqNo=19
L:1214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
M:341 Repeated in SeqNo=23
L:1250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:96
L:1264 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1268 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25
L:1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:60
M:341 Repeated in SeqNo=25
L:1312 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1316 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29
L:1317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:1327 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1331 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:1332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
```